

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 4, at the end of the application.

REMARKS

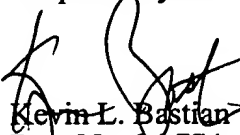
Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-3, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Abstract by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph [45] beginning at line 23 of page 6 has been amended as follows:

[45] The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (SEQ ID NO:3) (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Paragraph (TABLE 2) beginning at line 5 of page 96 has been amended as follows:

TABLE 2 CBF9 DNA and Protein Sequences

CBF9 DNA sequence (SEQ ID NO:1)

Gene name: ESTs
Unigene number: Hs.157601
Probeset Accession #: W07459
Nucleic Acid Accession #: AC005383
Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
TTTTATTTGC	AGACCTGGGC	CGATGCCGCT	TTAAAAAACG	CGAGGGGCTC	TATGCACCTC	120
CCTGGCGGTA	GTTCTCCGA	CCTCAGCCGG	GTCGGGTCGT	GCCGCCCTCT	CCCAGGAGAG	180
ACAAACAGGT	GTCCACGTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
TCGCCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GGCCGTCTGT	360
GTTTTCCTGT	TTTCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
GAAACCATCG	GGAAGATTTT	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
GCATTCCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCCCT	TGGATTCAAT	TTCAACCCAA	660
CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA	720
CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
CAGATCCTCA	TCATCGTCAC	TGATGGGAAG	TCCCAGGGGG	ATGTGGCACT	GCCATCCAAG	840
CAGCTGAAGG	AAAGGGGTGT	CAGTGTGTTT	CTGTGCGGGG	TCAGGTTTCC	CAGGTGGGAG	900
GAGCTGCATG	CAGTGGCCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTTGGC	TGAGCAGGTG	960
GAGGATGCCA	CCAACGGCCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
ACGCCAGACT	GCAGGGTCGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
GAGTTGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCCTTGC	GGTGCTGGCT	1140
GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCACCCTGC	CACCTGTCTAC	1200
AGGACCACCT	GCCCAGGCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
CCAGAAGGAC	TGGACGGCTA	CCAGTGCCCT	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	1320
TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTCGACCTCC	TCTTCCTGCT	GGACAGCTCT	1380
GCGGGCACCA	CTCTGGACGG	CTTCCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTTTGTGCGG	1440
GCCGTGCTGA	GCGAGGACTC	TCGGGCCCCA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
CTGGTGGCGG	TGCCTGTGGG	GGAGTACCAG	GATGTGCCTG	ACCTGGTCTG	GAGCCTCGAT	1560
GGCATTCCCT	TCCGTGGTGG	CCCCACCCTG	ACGGGCAGTG	CCTTGCGGCA	GGCGGCAGAG	1620
CGTGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTGG	1680
CTCACTGAGT	CACACTCCGA	GGATGAGGTT	CGCGGCCACG	CGCGTCACGC	AAGGGCGCGA	1740
GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
GAGTGCAGG	GGAAGCTGTG	CAGCCGGCAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
AGCTTTGTGT	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCGGC	2040
CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	GCCTTCGGGC	TGGACACCAA	ACCCACCCGG	2100
GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCCTGGT	2220

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GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCTT 2280
GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA 2340
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GCCGACCTGC GGTACCACCA GGACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460
CCAGTCAACC TCTGCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAT 2520
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ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCCTG 2700
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TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
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TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA 3000
CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG 3060
AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGCAG 3120
GCCACTTTTC CACTTCCCCA GAGACATTCT GGATGCATTG GCATTGAGTC TGAAAGGGGG 3180
CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGAAAA 3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360
ACCTTGAAGG TCTTC

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CBF9 Protein sequence (SEQ ID NO:2)

Gene name: ESTs
Unigene number: Hs.157601

Protein Accession #: none found

Signal sequence: 1-17
Transmembrane domains: none found
VGW domains: 49-223; 341-518; 529-706
EGF domains: 298-333; 715-748
Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPWR EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL 360
RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLGVGS 480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQKLCSS QRPQCRTQAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLNRNGI 660
SVLVVGVGPV LSEGLRRLAG PRDSLIVHAA YADLRHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

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